Amendment to the Claims:

Please amend the claims as follows:

Please cancel claims 2 to 45, 47 to 52, 54, 55, 59, 60, 62, 63, 65, 67, 69, 71, 72, 74 to 107, 108 to 124, 127 to 129, 132, 134, 136, 139, 141 to 156, 158 to 160, 162 to 168, 170, 172 to 217, 219 to 220, 222 to 224, 226 to 228, 230, 235, 237 to 240, 242 to 261, 263 to 264, 266 to 268 and 270 without prejudice or disclaimer.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): An isolated, synthetic or recombinant nucleic acid comprising

(a) a nucleic acid sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO:5 over a region of at least about 100, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 or more residues, or to the full length of SEQ ID NO:5;

a nucleic acid sequence having at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO:7 over a region of at least about 100, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 or more residues, or to the full length of SEQ ID NO:7;

a nucleic acid sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO:11 over a region of at least about 100, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 or more residues, or to the full length of SEQ ID NO:11;

a nucleic acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO:13 over a region of at least about 100, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 or more residues, or or to the full length of SEQ ID NO:13; or

a nucleic acid sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO:15 over a region of at least about 100, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 or more residues, or to the full length of SEQ ID NO:15;

wherein the nucleic acid encodes at least one polypeptide having an amylase activity, and optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection,

wherein optionally the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default; or

(b) a nucleic acid sequence encoding a polypeptide having the sequence of SEQ ID NO:2, a polypeptide having the sequence of SEQ ID NO:6, a polypeptide having the sequence of SEQ ID NO:8, a polypeptide having the sequence of SEQ ID NO:12, a polypeptide having the sequence of SEQ ID NO:14, or a polypeptide having the sequence of SEQ ID NO:16; or

(c) a nucleic acid sequence that hybridizes under stringent conditions to a nucleic acid comprising the sequence of SEQ ID NO:1, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:15, wherein the nucleic acid encodes a polypeptide having an amylase activity, wherein the nucleic acid sequence is about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 residues in length or the full length of a gene or transcript,

wherein the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes; or

(d) a sequence fully complementary to (a), (b) or (c),

wherein optionally the amylase activity comprises: hydrolyzing glucosidic bonds; a glucoamylase activity; a 1,4-α-D-glucan glucohydralase activity; an α-amylase activity; an exoamylase activity; a β-amylase activity; hydrolyzing an α-1,4-glucosidic bond; hydrolyzing an α-1,6-glucosidic bond; hydrolyzing glucosidic bonds in a starch; hydrolyzing glucosidic bonds in the starch to produce maltodextrines; cleaving a maltose or a D-glucose unit from non-reducing end of the starch;

wherein optionally the amylase activity is thermostable; or the amylase activity comprises retaining an amylase activity under conditions comprising a temperature range of between about 37°C to about 95°C; or the amylase activity comprises retaining an amylase activity under conditions comprising a temperature range of between about 55°C to about 85°C; or the amylase activity comprises retaining an amylase activity under conditions comprising a temperature range of between about 70°C to about 95°C; or the amylase activity comprises retaining an amylase activity under conditions comprising a temperature range of between about 90°C to about 95°C;

wherein optionally the amylase activity is thermotolerant; or the amylase activity comprises retaining an amylase activity after exposure to a temperature in the range from greater than 37°C to about 95°C; or the amylase activity comprises retaining an amylase activity after exposure to a temperature in the range from greater than 55°C to about 85°C; or the amylase activity comprises retaining an amylase activity after exposure to a temperature in the range from greater than 90°C to about 95°C.

Claims 2 to 45 (canceled)

Claims 46 (amended): A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with an amylase activity, wherein the probe comprises at least 10 consecutive bases of a sequence comprising: (a) the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:1, the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:5, the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:7, the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:11, the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:13, or the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:15, or (b) the nucleic acid sequence of claim 1; wherein the probe identifies the nucleic acid by binding or hybridization,

wherein optionally the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of the nucleic acid sequence of (a) or (b),

wherein optionally the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of the nucleic acid sequence of (a) or (b).

Claims 47 to 52 (canceled)

Claim 53 (amended): An amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide having an amylase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising: (a) the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:1, or a subsequence thereof, the sequence of SEQ ID NO:5, or a subsequence thereof, the [[a]] sequence of ~~as set forth~~

~~in~~ SEQ ID NO:7, or a subsequence thereof, the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:11, or a subsequence thereof, the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:13, or a subsequence thereof, the [[a]] sequence of ~~as set forth in~~ SEQ ID NO:15, or a subsequence thereof, or (b) the nucleic acid sequence of claim 1;

wherein optionally each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence.

Claims 54 and 55 (canceled)

Claim 56 (amended): An expression cassette comprising a nucleic acid comprising the nucleic acid sequence of claim 1~~:~~

~~(i) a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:5, or a subsequence thereof, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof, a sequence as set forth in SEQ ID NO:11, or a subsequence thereof, a sequence as set forth in SEQ ID NO:13, or a subsequence thereof, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof~~.

Claim 57 (amended): A vector comprising a nucleic acid comprising the nucleic acid sequence of claim 1

~~(i) a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:5, or a subsequence thereof, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof, a sequence as set forth in SEQ ID NO:11, or a subsequence thereof, a sequence as set forth in SEQ ID NO:13, or a subsequence thereof, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof~~.

Claim 58 (amended): A cloning vehicle comprising a vector as set forth in claim 57, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome,

wherein optionally the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector, or, comprises a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

Claims 59 and 60 (canceled)

Claim 61 (amended): A transformed cell comprising the [[a]] vector of claim 57, or the nucleic acid of claim 1 ~~, wherein the vector comprises~~

~~(i) a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:5, or a subsequence thereof, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof, a sequence as set forth in SEQ ID NO:11, or a subsequence thereof, a sequence as set forth in SEQ ID NO:13, or a subsequence thereof, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof~~, wherein optionally the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

Claims 62 and 63 (canceled)

Claim 64 (currently amended): A transgenic non-human animal comprising the vector of claim 57, or the nucleic acid of claim 1

~~(i) a nucleic acid sequence as set forth in SEQ ID NO:1,~~

~~a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:5, or a subsequence thereof, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof, a sequence as set forth in SEQ ID NO:11, or a subsequence thereof, a sequence as set forth in SEQ ID NO:13, or a subsequence thereof, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof~~, wherein optionally the animal is a mouse, a goat, a rabbit, a sheep, a pig, a cows or a rat.

Claim 65 (canceled)

Claim 66 (currently amended): A transgenic plant comprising the vector of claim 57, or the nucleic acid of claim 1

~~(i) a nucleic acid sequence as set forth in SEQ ID NO:1,~~

~~a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:5, or a subsequence thereof, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof, a sequence as set forth in SEQ ID NO:11, or a subsequence thereof, a sequence as set forth in SEQ ID NO:13, or a subsequence thereof, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof~~, wherein optionally the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

Claim 67 (canceled)

Claim 68 (currently amended): A transgenic seed comprising the vector of claim 57, or the nucleic acid of claim 1

~~(i) a nucleic acid sequence as set forth in SEQ ID NO:1,~~

~~a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:5, or a subsequence thereof, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof, a sequence as set forth in SEQ ID NO:11, or a subsequence thereof, a sequence as set forth in SEQ ID NO:13, or a subsequence thereof, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof~~, wherein optionally the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

Claim 69 (canceled)

Claim 70 (currently amended): An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to the sequence of claim 1,

~~(i) a sequence as set forth in SEQ ID NO:1, or a subsequence thereof,~~

~~a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:5, or a subsequence thereof, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof, a sequence as set forth in SEQ ID NO:11, or a subsequence thereof, a sequence as set forth in SEQ ID NO:13, or a subsequence thereof, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof~~

wherein optionally the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

Claims 71 and 72 (canceled)

Claim 73 (currently amended): An isolated, synthetic or recombinant polypeptide comprising

(a) ~~a polypeptide comprising~~ an amino acid sequence as set forth in SEQ ID NO:2,

an amino acid sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO:6 over a region of at least about 50, 60, 70, 80, 90, 100, 200, 300, 400, 500 or more residues,

an amino acid sequence having at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID NO:8 over a region of at least about 50, 60, 70, 80, 90, 100, 200, 300, 400, 500 or more residues,

an amino acid sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID NO:12 over a region of at least about 50, 60, 70, 80, 90, 100, 200, 300, 400, 500 or more residues,

an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID NO:14 over a region of at least about 50, 60, 70, 80, 90, 100, 200, 300, 400, 500 or more residues, or

an amino acid sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID NO:16 over a region of at least about 50, 60, 70, 80, 90, 100, 200, 300, 400, 500 or more residues, or

(b) a polypeptide encoded by the [[a]] nucleic acid of claim 1 ~~comprising~~

~~(i) a nucleic acid sequence as set forth in SEQ ID NO:1,~~

~~a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 60% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,~~

~~a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues, or~~

~~a nucleic acid sequence having at least 80% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,~~

~~wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection; or,~~

~~(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:5, or a subsequence thereof, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof, a sequence as set forth in SEQ ID NO:11, or a subsequence thereof, a sequence as set forth in SEQ ID NO:13, or a subsequence thereof, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof~~

wherein the polypeptide has an amylase activity,

wherein optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection,

wherein optionally the amylase activity comprises: hydrolyzing glucosidic bonds; a glucoamylase activity; a 1,4-α-D-glucan glucohydralase activity; an α-amylase activity; an exoamylase activity; a β-amylase activity; hydrolyzing an α-1,4-glucosidic bond; hydrolyzing an α-1,6-glucosidic bond; hydrolyzing glucosidic bonds in a starch; hydrolyzing glucosidic bonds in the starch to produce maltodextrines; cleaving a maltose or a D-glucose unit from non-reducing end of the starch;

wherein optionally the amylase activity is thermostable; or the amylase activity comprises retaining an amylase activity under conditions comprising a temperature range of between about 37°C to about 95°C; or the amylase activity comprises retaining an amylase activity under conditions comprising a temperature range of between about 55°C to about 85°C; or the amylase activity comprises retaining an amylase activity under conditions comprising a temperature range of between about 70°C to about 95°C; or the amylase activity comprises retaining an amylase activity under conditions comprising a temperature range of between about 90°C to about 95°C;

wherein optionally the amylase activity is thermotolerant; or the amylase activity comprises retaining an amylase activity after exposure to a temperature in the range from greater than 37°C to about 95°C; or the amylase activity comprises retaining an amylase activity after exposure to a temperature in the range from greater than 55°C to about 85°C; or the amylase activity comprises retaining an amylase activity after exposure to a temperature in the range from greater than 90°C to about 95°C,

wherein optionally the amylase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, or optionally the amylase activity comprises a specific activity from about 500 to about 750 units per milligram of protein,

wherein optionally the polypeptide comprises at least one glycosylation site,

wherein optionally the polypeptide retains an amylase activity under conditions comprising about pH 5, about pH 4.5, about pH 8.0, about pH 8.5, about pH 9, about pH 9.5, about pH 10 or about pH 10.5.

Claims 74 to 106 (canceled)

Claim 107 (currently amended): An isolated or recombinant polypeptide comprising the polypeptide as set forth in claim 73 and lacking a signal sequence, or lacking an endogenous signal sequence and comprising a heterologous signal sequence, or further comprising a heterologous peptide or polypeptide.

Claims 108 to 124 (canceled)

Claim 125 (original): A protein preparation comprising a polypeptide as set forth in claim 73, wherein the protein preparation comprises a liquid, a solid or a gel.

Claim 126 (currently amended): A heterodimer comprising a polypeptide as set forth in claim 73 and a second domain,

wherein optionally the second domain is a polypeptide and the heterodimer is a fusion protein, or optionally the second domain is an epitope or a tag.

Claims 127 to 129 (canceled)

Claim 130 (currently amended): A homodimer comprising a polypeptide as set forth in claim 73.

Claim 131 (currently amended): An immobilized polypeptide comprising the ~~having an amylase activity, wherein the polypeptide comprises a~~ sequence of ~~as set forth in~~ claim 73 or claim 126,

wherein optionally the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

Claim 132 (canceled)

Claim 133 (currently amended): An array comprising (a) an immobilized polypeptide as set forth in claim 73 or claim 126, (b) an immobilized nucleic acid as set forth in claim 1, or (c) a combination thereof.

Claim 134 (canceled)

Claim 135 (currently amended): An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 73 or to a polypeptide encoded by a nucleic acid as set forth in claim 1 ~~or claim 41~~,

wherein optionally the antibody is a monoclonal or a polyclonal antibody.

Claim 136 (canceled)

Claim 137 (currently amended): A hybridoma comprising an antibody that specifically binds to the [[a]] polypeptide of ~~as set forth in~~ claim 73 or to a polypeptide encoded by a nucleic acid as set forth in claim 1 ~~or claim 41~~.

Claim 138 (currently amended): A food, feed, food supplement or feed supplement for an animal comprising:

the [[a]] polypeptide of ~~as set forth in~~ claim 73;

~~a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof,~~

wherein optionally the polypeptide is glycosylated.

Claim 139 (canceled)

Claim 140 (currently amended): An edible enzyme delivery matrix comprising:

the [[a]] polypeptide of ~~as set forth in~~ claim 73;

~~a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof,~~

wherein optionally the delivery matrix comprises a pellet, or the polypeptide is glycosylated, or the amylase activity is thermotolerant or thermostable.

Claims 141 to 156 (canceled)

Claim 157 (currently amended): A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises the sequence of ~~as set forth in~~ claim 73, a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41~~,

wherein optionally the system further comprises a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon,

wherein optionally the sequence comparison algorithm comprises a computer program that indicates polymorphisms,

wherein optionally the system further comprises an identifier that identifies one or more features in said sequence.

Claims 158 to 160 (canceled)

Claim 161 (currently amended): A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises the [[a]] polypeptide of ~~as set forth in~~ claim 73; a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41~~.

Claims 162 to 168 (canceled)

Claim 169 (currently amended): A method for isolating or recovering a nucleic acid encoding a polypeptide with an amylase activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising the [[a]] sequence of ~~as set forth in~~ claim 1 ~~or claim 41 or a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:9~~, or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with an amylase activity from an environmental sample,

wherein optionally the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample, or optionally the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

Claim 170 (canceled)

Claim 171 (currently amended): A method of generating a variant of a nucleic acid encoding a polypeptide with an amylase activity comprising the steps of:

(a) providing a template nucleic acid comprising the [[a]] sequence of ~~as set forth in~~ claim 1 ~~or claim 41 or a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, or SEQ ID NO:9~~; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid,

wherein optionally the method further comprises expressing the variant nucleic acid to generate a variant amylase polypeptide, or optionally the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturation mutagenesis (GSSM), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof,

wherein optionally the method is iteratively repeated until an amylase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced, or optionally the variant amylase polypeptide is thermotolerant and retains some activity after being exposed to an elevated temperature, or optionally the variant amylase polypeptide has increased glycosylation as compared to the amylase encoded by a template nucleic acid, or optionally the variant amylase polypeptide has an amylase activity under a high temperature, wherein the amylase encoded by the template nucleic acid is not active under the high temperature, or optionally the method is iteratively repeated until an amylase coding sequence having an altered codon usage from that of the template nucleic acid is produced, or optionally the

method is iteratively repeated until an amylase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

Claims 172 to 217 (canceled)

Claim 218 (currently amended): A method for hydrolyzing a starch comprising the following steps:

(a) providing a polypeptide having an amylase activity, wherein the polypeptide comprises the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide hydrolyzes the starch,

wherein optionally the composition comprises an α-1,4-glucosidic bond, or optionally the composition comprises an α-1,6-glucosidic bond.

Claims 219 to 220 (canceled)

Claim 221 (currently amended): A method for liquefying or removing a starch from a composition comprising the following steps:

(a) providing a polypeptide having an amylase activity, wherein the polypeptide comprises the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide removes or liquefies the starch.

Claims 222 to 224 (canceled)

Claim 225 (currently amended): A detergent composition comprising the [[a]] polypeptide of ~~as set forth in~~ claim 73; a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41; a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~, wherein the polypeptide comprises an amylase activity,

wherein optionally the amylase is a nonsurface-active amylase, or optionally the amylase is a surface-active amylase.

Claims 226 to 228 (canceled)

Claim 229 (currently amended): A method for hydrolyzing a starch in a feed or a food prior to consumption by an animal comprising the following steps:

(a) obtaining a feed material comprising a starch, wherein the starch can be hydrolyzed by a polypeptide having an amylase activity, wherein the polypeptide comprises:

the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~; and

(b) adding the polypeptide of step (a) to the feed or food material in an amount sufficient for a sufficient time period to cause hydrolysis of the starch and formation of a treated food or feed, thereby hydrolyzing the starch in the food or the feed prior to consumption by the animal,

wherein optionally the food or feed comprises rice, corn, barley, wheat, legumes, or potato.

Claim 230 (canceled)

Claim 231 (currently amended): A method for textile processing or desizing comprising the following steps:

(a) providing a polypeptide having an amylase activity, wherein the polypeptide comprises

the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under~~

~~stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~;

(b) providing a fabric; and

(c) contacting the polypeptide of step (a) and the fabric of step (b) under conditions wherein the amylase can process or desize the fabric.

Claim 232 (currently amended): A method for paper, fiber or pulp processing or deinking comprising the following steps:

(a) providing a polypeptide having an amylase activity, wherein the polypeptide comprises:

the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~;

(b) providing a composition comprising paper, pulp or fiber; and

(c) contacting the polypeptide of step (a) and the composition of step (b) under conditions wherein the polypeptide can process or deink the paper, pulp or fiber.

Claim 233 (currently amended): A method for treatment of lignocellulosic fibers comprising the following steps:

(a) providing a polypeptide having an amylase activity, wherein the polypeptide comprises

the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~;

(b) providing a lignocellulosic fiber; and

(c) contacting the polypeptide of step (a) and the fiber of step (b) under conditions wherein the polypeptide can treat the fiber thereby improving the fiber properties.

Claim 234 (currently amended): A method for producing a high-maltose or a high-glucose syrup comprising the following steps:

(a) providing a polypeptide having an amylase activity, wherein the polypeptide comprises the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~;

(b) providing a composition comprising a starch; and

(c) contacting the polypeptide of step (a) and the fabric of step (b) under conditions wherein the polypeptide of step (a) can hydrolyze the composition of step (b), thereby producing a high-maltose or a high-glucose syrup,

wherein optionally the starch is from rice, corn, barley, wheat, legumes, potato, or sweet potato.

Claim 235 (canceled)

Claim 236 (currently amended): A drilling process, or a method for improving the flow of the starch-containing production fluids, comprising the following steps:

(a) providing a polypeptide having an amylase activity, wherein the polypeptide comprises the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~;

(b) providing production fluid comprising a starch; and

(c) contacting the polypeptide of step (a) and the production fluid of step (b) under conditions wherein the amylase can hydrolyze the starch in the production fluid, thereby improving its flow by decreasing its density,

wherein optionally the production fluid is from a subterranean formation.

Claim 237 to 240 (canceled)

Claim 241 (currently amended): A method for using amylase in brewing or alcohol production comprising the following steps:

(a) providing a polypeptide comprising

the [[a]] polypeptide of ~~as set forth in~~ claim 73; or

a polypeptide encoded by the [[a]] nucleic acid of ~~as set forth in~~ claim 1 ~~or claim 41;~~

~~a polypeptide comprising an amino acid sequence having at least 90% identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:10 over a region of at least about 100 residues; or~~

~~a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence having at least 90% identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:9 or a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof, a sequence as set forth in SEQ ID NO:3, or a subsequence thereof, a sequence as set forth in SEQ ID NO:9, or a subsequence thereof~~;

(b) providing a composition used for brewing or in alcohol production comprising a starch;

(c) combining the polypeptide of step (a) with the composition of the step (b) under conditions wherein the polypeptide can hydrolyze the starch in the composition used for brewing or alcohol production.

Claims 242 to 261 (canceled)

Claim 262 (currently amended): An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having an amylase activity, wherein the primer pair is capable of amplifying a nucleic acid comprising the [[a]] nucleic acid sequence of ~~as set forth in~~ claim 1 ~~or claim 24~~, or a subsequence thereof,

wherein optionally a member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence,

or optionally the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the sequence of claim 1, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the complementary strand of the first member.

Claims 263 to 264 (canceled)

Claim 265 (currently amended): An isolated, synthetic or recombinant amylase-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim [[264]] 262, wherein optionally the amplification is by polymerase chain reaction (PCR), or optionally the nucleic acid generated by amplification of a gene library, and optionally the gene library is an environmental library.

Claims 266 to 268 (canceled)

Claim 269 (currently amended): An isolated, synthetic or recombinant protease encoded by a protease-encoding nucleic acid as set forth in claim 265.

Claim 270 (canceled)

Claim 271 (new): A method for producing a food or feed comprising a recombinant amylase, the method comprising the steps of:

(a) providing a polypeptide having an amylase activity, wherein the polypeptide comprises the polypeptide of claim 73 or a polypeptide encoded by the nucleic acid of claim 1;

(b) providing a composition comprising a food or feed;

(c) expressing the nucleic acid to produce a recombinant amylase; and

(d) mixing the recombinant amylase and the feed-comprising composition, thereby producing a food or feed comprising a recombinant amylase.

Claim 272 (new): A corn wet milling process comprising use of a polypeptide having amylase activity, wherein the polypeptide comprises the polypeptide of claim 73 or a polypeptide encoded by the nucleic acid of claim 1, wherein optionally the process further comprises use of a second polypeptide having amylase activity, an alpha amylase activity, or a beta amylase, or another enzyme.

Claim 273 (new): A baking process comprising use of a polypeptide having amylase activity, wherein the polypeptide comprises the polypeptide of claim 73 or a polypeptide encoded by the nucleic acid of claim 1, wherein optionally the baking process further comprises use of a second polypeptide having an amylase activity, an alpha amylase activity, or a beta amylase, or another enzyme.